

WEST Search History

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DATE: Friday, December 17, 2004

| Hide? | Set Name | Query | Hit Count |
|--------------------------|-----------------|---|------------------|
| | | <i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i> | |
| <input type="checkbox"/> | L16 | L15 and l7 | 0 |
| <input type="checkbox"/> | L15 | L14 and l9 | 0 |
| <input type="checkbox"/> | L14 | (530/387.1,387.9,388.24,389.1,389.2)![CCLS] | 3631 |
| <input type="checkbox"/> | L13 | L12 and l11 | 1 |
| <input type="checkbox"/> | L12 | antibod\$.clm. | 35412 |
| <input type="checkbox"/> | L11 | L10 and l7 | 4 |
| <input type="checkbox"/> | L10 | L9 or l8 | 13 |
| <input type="checkbox"/> | L9 | PARG.ab. | 13 |
| <input type="checkbox"/> | L8 | PARG.ti. | 8 |
| <input type="checkbox"/> | L7 | L6 or l5 | 3843 |
| <input type="checkbox"/> | L6 | ame.in. | 995 |
| <input type="checkbox"/> | L5 | jacobson.in. | 2852 |
| <input type="checkbox"/> | L4 | l3 or l2 or l1 | 3 |
| <input type="checkbox"/> | L3 | 6333148.pn. | 1 |
| <input type="checkbox"/> | L2 | 6337202.pn. | 1 |
| <input type="checkbox"/> | L1 | 6395543.pn. | 1 |

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 1.32945 Seconds
(without alignments)
1546.392 Million cell updates/sec

Title: US-09-973-451-11
Perfect score: 167
Sequence: 1 LFTEVLHDHNECLIITGTEQYSEYTGyaETyr 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | % | | | | | |
|--------|-------|-------|--------|----|------------------|-------------------|--|
| Result | | Query | | | | | |
| No. | Score | Match | Length | DB | ID | Description | |
| 1 | 167 | 100.0 | 31 | 3 | US-09-302-812-11 | Sequence 11, Appl | |
| 2 | 167 | 100.0 | 31 | 3 | US-09-511-477-11 | Sequence 11, Appl | |
| 3 | 167 | 100.0 | 31 | 3 | US-09-511-507-11 | Sequence 11, Appl | |
| 4 | 167 | 100.0 | 968 | 3 | US-09-302-812-6 | Sequence 6, Appli | |
| 5 | 167 | 100.0 | 968 | 3 | US-09-511-477-6 | Sequence 6, Appli | |
| 6 | 167 | 100.0 | 968 | 3 | US-09-511-507-6 | Sequence 6, Appli | |
| 7 | 167 | 100.0 | 976 | 3 | US-09-302-812-4 | Sequence 4, Appli | |
| 8 | 167 | 100.0 | 976 | 3 | US-09-511-477-4 | Sequence 4, Appli | |
| 9 | 167 | 100.0 | 976 | 3 | US-09-511-507-4 | Sequence 4, Appli | |
| 10 | 167 | 100.0 | 977 | 3 | US-09-302-812-2 | Sequence 2, Appli | |
| 11 | 167 | 100.0 | 977 | 3 | US-09-511-477-2 | Sequence 2, Appli | |

| | | | | | | |
|----|------|-------|------|---|----------------------|-------------------|
| 12 | 167 | 100.0 | 977 | 3 | US-09-511-507-2 | Sequence 2, Appli |
| 13 | 82 | 49.1 | 768 | 3 | US-09-302-812-8 | Sequence 8, Appli |
| 14 | 82 | 49.1 | 768 | 3 | US-09-511-477-8 | Sequence 8, Appli |
| 15 | 82 | 49.1 | 768 | 3 | US-09-511-507-8 | Sequence 8, Appli |
| 16 | 53.5 | 32.0 | 697 | 4 | US-09-540-236-3601 | Sequence 3601, Ap |
| 17 | 53 | 31.7 | 726 | 3 | US-09-302-812-10 | Sequence 10, Appl |
| 18 | 53 | 31.7 | 726 | 3 | US-09-511-477-10 | Sequence 10, Appl |
| 19 | 53 | 31.7 | 726 | 3 | US-09-511-507-10 | Sequence 10, Appl |
| 20 | 49.5 | 29.6 | 123 | 4 | US-09-107-532A-5299 | Sequence 5299, Ap |
| 21 | 49.5 | 29.6 | 434 | 4 | US-09-107-532A-4075 | Sequence 4075, Ap |
| 22 | 49 | 29.3 | 453 | 1 | US-08-374-155A-8 | Sequence 8, Appli |
| 23 | 49 | 29.3 | 453 | 2 | US-08-785-396-8 | Sequence 8, Appli |
| 24 | 48.5 | 29.0 | 122 | 4 | US-09-107-532A-5851 | Sequence 5851, Ap |
| 25 | 48.5 | 29.0 | 330 | 4 | US-09-540-236-3751 | Sequence 3751, Ap |
| 26 | 48 | 28.7 | 372 | 1 | US-08-597-236-8 | Sequence 8, Appli |
| 27 | 48 | 28.7 | 372 | 1 | US-08-746-682A-8 | Sequence 8, Appli |
| 28 | 48 | 28.7 | 408 | 4 | US-09-248-796A-19266 | Sequence 19266, A |
| 29 | 48 | 28.7 | 993 | 4 | US-09-894-998A-50 | Sequence 50, Appl |
| 30 | 48 | 28.7 | 1037 | 4 | US-09-894-998A-54 | Sequence 54, Appl |
| 31 | 48 | 28.7 | 1113 | 4 | US-09-894-998A-51 | Sequence 51, Appl |
| 32 | 46 | 27.5 | 230 | 4 | US-09-328-352-7134 | Sequence 7134, Ap |
| 33 | 46 | 27.5 | 542 | 4 | US-09-198-452A-1003 | Sequence 1003, Ap |
| 34 | 45.5 | 27.2 | 208 | 4 | US-09-248-796A-15775 | Sequence 15775, A |
| 35 | 45 | 26.9 | 168 | 3 | US-08-990-791-9 | Sequence 9, Appli |
| 36 | 45 | 26.9 | 168 | 4 | US-09-372-591-9 | Sequence 9, Appli |
| 37 | 45 | 26.9 | 192 | 4 | US-09-270-767-38002 | Sequence 38002, A |
| 38 | 45 | 26.9 | 192 | 4 | US-09-270-767-53219 | Sequence 53219, A |
| 39 | 45 | 26.9 | 226 | 4 | US-09-270-767-59161 | Sequence 59161, A |
| 40 | 45 | 26.9 | 342 | 4 | US-09-543-681A-6588 | Sequence 6588, Ap |
| 41 | 45 | 26.9 | 371 | 4 | US-09-270-767-43760 | Sequence 43760, A |
| 42 | 45 | 26.9 | 418 | 3 | US-08-844-054-2 | Sequence 2, Appli |
| 43 | 45 | 26.9 | 418 | 3 | US-09-347-333-2 | Sequence 2, Appli |
| 44 | 45 | 26.9 | 418 | 4 | US-09-583-110-4220 | Sequence 4220, Ap |
| 45 | 45 | 26.9 | 686 | 2 | US-08-993-228-12 | Sequence 12, Appl |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 4.45213 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-11
Perfect score: 167
Sequence: 1 LFTEVLHDHNECLIITGTEQYSEYTGyaETyr 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|----------------------|-------------------|
| 1 | 167 | 100.0 | 31 | 9 | US-09-973-451-11 | Sequence 11, Appl |
| 2 | 167 | 100.0 | 968 | 9 | US-09-973-451-6 | Sequence 6, Appli |
| 3 | 167 | 100.0 | 976 | 9 | US-09-973-451-4 | Sequence 4, Appli |
| 4 | 167 | 100.0 | 977 | 9 | US-09-973-451-2 | Sequence 2, Appli |
| 5 | 82 | 49.1 | 768 | 9 | US-09-973-451-8 | Sequence 8, Appli |
| 6 | 72 | 43.1 | 518 | 17 | US-10-425-115-239190 | Sequence 239190, |
| 7 | 72 | 43.1 | 546 | 15 | US-10-425-114-60000 | Sequence 60000, A |
| 8 | 71 | 42.5 | 509 | 16 | US-10-437-963-202306 | Sequence 202306, |
| 9 | 58 | 34.7 | 47 | 17 | US-10-425-115-325463 | Sequence 325463, |
| 10 | 56 | 33.5 | 300 | 15 | US-10-424-599-233915 | Sequence 233915, |
| 11 | 55 | 32.9 | 524 | 15 | US-10-425-114-65345 | Sequence 65345, A |
| 12 | 55 | 32.9 | 529 | 15 | US-10-425-114-65514 | Sequence 65514, A |
| 13 | 55 | 32.9 | 536 | 17 | US-10-425-115-244714 | Sequence 244714, |
| 14 | 55 | 32.9 | 542 | 17 | US-10-425-115-244717 | Sequence 244717, |
| 15 | 54.5 | 32.6 | 428 | 15 | US-10-282-122A-52564 | Sequence 52564, A |
| 16 | 53 | 31.7 | 726 | 9 | US-09-973-451-10 | Sequence 10, Appl |
| 17 | 52 | 31.1 | 87 | 17 | US-10-425-115-252508 | Sequence 252508, |
| 18 | 52 | 31.1 | 147 | 16 | US-10-437-963-138462 | Sequence 138462, |
| 19 | 50.5 | 30.2 | 86 | 16 | US-10-437-963-150772 | Sequence 150772, |
| 20 | 49.5 | 29.6 | 307 | 15 | US-10-282-122A-71975 | Sequence 71975, A |
| 21 | 49 | 29.3 | 224 | 15 | US-10-425-114-45983 | Sequence 45983, A |
| 22 | 49 | 29.3 | 225 | 16 | US-10-767-701-44091 | Sequence 44091, A |
| 23 | 49 | 29.3 | 329 | 15 | US-10-425-114-52216 | Sequence 52216, A |
| 24 | 49 | 29.3 | 427 | 15 | US-10-389-566-1764 | Sequence 1764, Ap |
| 25 | 49 | 29.3 | 447 | 15 | US-10-282-122A-72107 | Sequence 72107, A |
| 26 | 49 | 29.3 | 453 | 14 | US-10-061-269-8 | Sequence 8, Appli |
| 27 | 49 | 29.3 | 453 | 14 | US-10-463-509-8 | Sequence 8, Appli |
| 28 | 49 | 29.3 | 453 | 14 | US-10-463-569-8 | Sequence 8, Appli |
| 29 | 49 | 29.3 | 499 | 15 | US-10-424-599-229000 | Sequence 229000, |
| 30 | 49 | 29.3 | 519 | 17 | US-10-739-930-9479 | Sequence 9479, Ap |
| 31 | 49 | 29.3 | 1229 | 16 | US-10-437-963-141907 | Sequence 141907, |
| 32 | 48 | 28.7 | 101 | 15 | US-10-424-599-240498 | Sequence 240498, |
| 33 | 48 | 28.7 | 130 | 15 | US-10-425-114-49850 | Sequence 49850, A |
| 34 | 48 | 28.7 | 413 | 15 | US-10-389-566-1499 | Sequence 1499, Ap |
| 35 | 48 | 28.7 | 519 | 17 | US-10-425-115-200991 | Sequence 200991, |
| 36 | 48 | 28.7 | 993 | 9 | US-09-894-998-50 | Sequence 50, Appl |
| 37 | 48 | 28.7 | 993 | 14 | US-10-121-988-50 | Sequence 50, Appl |
| 38 | 48 | 28.7 | 993 | 14 | US-10-200-562-50 | Sequence 50, Appl |
| 39 | 48 | 28.7 | 993 | 14 | US-10-237-551-50 | Sequence 50, Appl |
| 40 | 48 | 28.7 | 1037 | 9 | US-09-894-998-54 | Sequence 54, Appl |
| 41 | 48 | 28.7 | 1037 | 14 | US-10-121-988-54 | Sequence 54, Appl |
| 42 | 48 | 28.7 | 1037 | 14 | US-10-200-562-54 | Sequence 54, Appl |
| 43 | 48 | 28.7 | 1037 | 14 | US-10-237-551-54 | Sequence 54, Appl |
| 44 | 48 | 28.7 | 1113 | 9 | US-09-894-998-51 | Sequence 51, Appl |
| 45 | 48 | 28.7 | 1113 | 14 | US-10-121-988-51 | Sequence 51, Appl |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 1.24368 Seconds
(without alignments)
1546.392 Million cell updates/sec

Title: US-09-973-451-12
Perfect score: 152
Sequence: 1 AYCGFLRPGVSSSENLSAVATGNXGCGAFG 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|-------|---------|--------|----|------------------|-------------------|
| | | Match | Length | | | |
| 1 | 150 | 98.7 | 29 | 3 | US-09-302-812-12 | Sequence 12, Appl |
| 2 | 150 | 98.7 | 29 | 3 | US-09-511-477-12 | Sequence 12, Appl |
| 3 | 150 | 98.7 | 29 | 3 | US-09-511-507-12 | Sequence 12, Appl |
| 4 | 149 | 98.0 | 976 | 3 | US-09-302-812-4 | Sequence 4, Appli |
| 5 | 149 | 98.0 | 976 | 3 | US-09-511-477-4 | Sequence 4, Appli |
| 6 | 149 | 98.0 | 976 | 3 | US-09-511-507-4 | Sequence 4, Appli |
| 7 | 149 | 98.0 | 977 | 3 | US-09-302-812-2 | Sequence 2, Appli |
| 8 | 149 | 98.0 | 977 | 3 | US-09-511-477-2 | Sequence 2, Appli |
| 9 | 149 | 98.0 | 977 | 3 | US-09-511-507-2 | Sequence 2, Appli |
| 10 | 144 | 94.7 | 968 | 3 | US-09-302-812-6 | Sequence 6, Appli |
| 11 | 144 | 94.7 | 968 | 3 | US-09-511-477-6 | Sequence 6, Appli |

| | | | | | | |
|----|------|------|------|---|----------------------|-------------------|
| 12 | 144 | 94.7 | 968 | 3 | US-09-511-507-6 | Sequence 6, Appli |
| 13 | 69 | 45.4 | 768 | 3 | US-09-302-812-8 | Sequence 8, Appli |
| 14 | 69 | 45.4 | 768 | 3 | US-09-511-477-8 | Sequence 8, Appli |
| 15 | 69 | 45.4 | 768 | 3 | US-09-511-507-8 | Sequence 8, Appli |
| 16 | 60.5 | 39.8 | 543 | 1 | US-08-375-709-17 | Sequence 17, Appl |
| 17 | 60.5 | 39.8 | 543 | 1 | US-08-752-929-17 | Sequence 17, Appl |
| 18 | 60.5 | 39.8 | 543 | 3 | US-09-090-793-10 | Sequence 10, Appl |
| 19 | 60.5 | 39.8 | 543 | 4 | US-09-231-899-10 | Sequence 10, Appl |
| 20 | 53 | 34.9 | 154 | 4 | US-09-270-767-39843 | Sequence 39843, A |
| 21 | 53 | 34.9 | 154 | 4 | US-09-270-767-55060 | Sequence 55060, A |
| 22 | 53 | 34.9 | 403 | 4 | US-09-170-496D-114 | Sequence 114, App |
| 23 | 53 | 34.9 | 403 | 4 | US-09-170-496D-224 | Sequence 224, App |
| 24 | 53 | 34.9 | 403 | 4 | US-09-743-742B-4 | Sequence 4, Appli |
| 25 | 53 | 34.9 | 403 | 4 | US-09-743-742B-10 | Sequence 10, Appl |
| 26 | 52 | 34.2 | 708 | 4 | US-09-248-796A-16456 | Sequence 16456, A |
| 27 | 50.5 | 33.2 | 411 | 4 | US-09-540-236-3549 | Sequence 3549, Ap |
| 28 | 49.5 | 32.6 | 726 | 3 | US-09-302-812-10 | Sequence 10, Appl |
| 29 | 49.5 | 32.6 | 726 | 3 | US-09-511-477-10 | Sequence 10, Appl |
| 30 | 49.5 | 32.6 | 726 | 3 | US-09-511-507-10 | Sequence 10, Appl |
| 31 | 49 | 32.2 | 1196 | 4 | US-09-252-991A-18261 | Sequence 18261, A |
| 32 | 48.5 | 31.9 | 887 | 4 | US-09-077-940A-2 | Sequence 2, Appli |
| 33 | 47.5 | 31.2 | 298 | 3 | US-09-025-691-1 | Sequence 1, Appli |
| 34 | 46.5 | 30.6 | 134 | 4 | US-09-621-976-4066 | Sequence 4066, Ap |
| 35 | 46.5 | 30.6 | 307 | 3 | US-09-049-672A-9 | Sequence 9, Appli |
| 36 | 46 | 30.3 | 359 | 2 | US-08-713-636-2 | Sequence 2, Appli |
| 37 | 46 | 30.3 | 681 | 1 | US-08-083-590A-18 | Sequence 18, Appl |
| 38 | 46 | 30.3 | 681 | 2 | US-08-346-128-37 | Sequence 37, Appl |
| 39 | 46 | 30.3 | 681 | 3 | US-08-532-384-18 | Sequence 18, Appl |
| 40 | 46 | 30.3 | 1068 | 1 | US-08-537-210A-2 | Sequence 2, Appli |
| 41 | 46 | 30.3 | 1068 | 3 | US-09-113-825-2 | Sequence 2, Appli |
| 42 | 46 | 30.3 | 1078 | 1 | US-08-264-534-32 | Sequence 32, Appl |
| 43 | 46 | 30.3 | 1078 | 1 | US-08-083-590A-11 | Sequence 11, Appl |
| 44 | 46 | 30.3 | 1078 | 1 | US-08-465-500-32 | Sequence 32, Appl |
| 45 | 46 | 30.3 | 1078 | 2 | US-08-346-128-32 | Sequence 32, Appl |

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 4.16489 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-12
Perfect score: 152
Sequence: 1 AYCGFLRPGVSSSENLSAVATGNXGCCAFG 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|-------|----------------|--------|----|----------------------|-------------------|
| 1 | 150 | 98.7 | 29 | 9 | US-09-973-451-12 | Sequence 12, Appl |
| 2 | 149 | 98.0 | 976 | 9 | US-09-973-451-4 | Sequence 4, Appli |
| 3 | 149 | 98.0 | 977 | 9 | US-09-973-451-2 | Sequence 2, Appli |
| 4 | 144 | 94.7 | 968 | 9 | US-09-973-451-6 | Sequence 6, Appli |
| 5 | 74 | 48.7 | 509 | 16 | US-10-437-963-202306 | Sequence 202306, |
| 6 | 69 | 45.4 | 768 | 9 | US-09-973-451-8 | Sequence 8, Appli |
| 7 | 67 | 44.1 | 518 | 17 | US-10-425-115-239190 | Sequence 239190, |
| 8 | 67 | 44.1 | 546 | 15 | US-10-425-114-60000 | Sequence 60000, A |
| 9 | 66 | 43.4 | 180 | 15 | US-10-424-599-156445 | Sequence 156445, |
| 10 | 60.5 | 39.8 | 543 | 14 | US-10-331-061-10 | Sequence 10, Appl |
| 11 | 57 | 37.5 | 104 | 17 | US-10-425-115-239179 | Sequence 239179, |
| 12 | 55.5 | 36.5 | 768 | 14 | US-10-369-493-2214 | Sequence 2214, Ap |
| 13 | 53 | 34.9 | 75 | 9 | US-09-993-844-46 | Sequence 46, Appl |
| 14 | 53 | 34.9 | 75 | 15 | US-10-633-438-32 | Sequence 32, Appl |
| 15 | 53 | 34.9 | 403 | 14 | US-10-251-385-114 | Sequence 114, App |
| 16 | 53 | 34.9 | 403 | 14 | US-10-251-385-224 | Sequence 224, App |
| 17 | 53 | 34.9 | 403 | 14 | US-10-225-567A-540 | Sequence 540, App |
| 18 | 53 | 34.9 | 403 | 14 | US-10-290-078-18 | Sequence 18, Appl |
| 19 | 53 | 34.9 | 403 | 14 | US-10-353-690-10 | Sequence 10, Appl |
| 20 | 53 | 34.9 | 422 | 16 | US-10-367-094-141 | Sequence 141, App |
| 21 | 53 | 34.9 | 426 | 15 | US-10-311-671-1 | Sequence 1, Appli |
| 22 | 53 | 34.9 | 445 | 14 | US-10-240-145-53 | Sequence 53, Appl |
| 23 | 53 | 34.9 | 445 | 14 | US-10-240-145-139 | Sequence 139, App |
| 24 | 53 | 34.9 | 2762 | 14 | US-10-123-155-13 | Sequence 13, Appl |
| 25 | 53 | 34.9 | 2762 | 14 | US-10-146-731-13 | Sequence 13, Appl |
| 26 | 53 | 34.9 | 2762 | 14 | US-10-140-472-13 | Sequence 13, Appl |
| 27 | 53 | 34.9 | 2762 | 14 | US-10-141-761-13 | Sequence 13, Appl |
| 28 | 53 | 34.9 | 2762 | 14 | US-10-142-885-13 | Sequence 13, Appl |
| 29 | 53 | 34.9 | 2762 | 14 | US-10-158-790-13 | Sequence 13, Appl |
| 30 | 53 | 34.9 | 2762 | 14 | US-10-137-871-13 | Sequence 13, Appl |
| 31 | 53 | 34.9 | 2762 | 14 | US-10-140-923-13 | Sequence 13, Appl |
| 32 | 53 | 34.9 | 2762 | 14 | US-10-141-756-13 | Sequence 13, Appl |
| 33 | 53 | 34.9 | 2762 | 14 | US-10-141-759-13 | Sequence 13, Appl |
| 34 | 53 | 34.9 | 2762 | 14 | US-10-140-805-13 | Sequence 13, Appl |
| 35 | 53 | 34.9 | 2762 | 14 | US-10-140-864-13 | Sequence 13, Appl |
| 36 | 53 | 34.9 | 2762 | 15 | US-10-142-426-13 | Sequence 13, Appl |
| 37 | 52 | 34.2 | 181 | 15 | US-10-424-599-177700 | Sequence 177700, |
| 38 | 51 | 33.6 | 114 | 17 | US-10-425-115-321774 | Sequence 321774, |
| 39 | 51 | 33.6 | 315 | 16 | US-10-437-963-157064 | Sequence 157064, |
| 40 | 51 | 33.6 | 371 | 14 | US-10-369-493-19533 | Sequence 19533, A |
| 41 | 51 | 33.6 | 379 | 9 | US-09-738-626-5142 | Sequence 5142, Ap |
| 42 | 50.5 | 33.2 | 501 | 15 | US-10-282-122A-63359 | Sequence 63359, A |
| 43 | 50 | 32.9 | 130 | 17 | US-10-425-115-247900 | Sequence 247900, |
| 44 | 50 | 32.9 | 199 | 16 | US-10-437-963-180011 | Sequence 180011, |
| 45 | 50 | 32.9 | 372 | 15 | US-10-424-599-269980 | Sequence 269980, |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 0.471742 Seconds
(without alignments)
1546.392 Million cell updates/sec

Title: US-09-973-451-13
Perfect score: 53
Sequence: 1 FLINPELIVSR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | | DB | ID | Description |
|------------|-------|-------|--------|----|------------------|-------------------|
| | | Match | Length | | | |
| 1 | 53 | 100.0 | 11 | 3 | US-09-302-812-13 | Sequence 13, Appl |
| 2 | 53 | 100.0 | 11 | 3 | US-09-511-477-13 | Sequence 13, Appl |
| 3 | 53 | 100.0 | 11 | 3 | US-09-511-507-13 | Sequence 13, Appl |
| 4 | 53 | 100.0 | 968 | 3 | US-09-302-812-6 | Sequence 6, Appli |
| 5 | 53 | 100.0 | 968 | 3 | US-09-511-477-6 | Sequence 6, Appli |
| 6 | 53 | 100.0 | 968 | 3 | US-09-511-507-6 | Sequence 6, Appli |
| 7 | 53 | 100.0 | 977 | 3 | US-09-302-812-2 | Sequence 2, Appli |
| 8 | 53 | 100.0 | 977 | 3 | US-09-511-477-2 | Sequence 2, Appli |
| 9 | 53 | 100.0 | 977 | 3 | US-09-511-507-2 | Sequence 2, Appli |
| 10 | 52 | 98.1 | 976 | 3 | US-09-302-812-4 | Sequence 4, Appli |
| 11 | 52 | 98.1 | 976 | 3 | US-09-511-477-4 | Sequence 4, Appli |

| | | | | | | |
|----|----|------|------|---|----------------------|-------------------|
| 12 | 52 | 98.1 | 976 | 3 | US-09-511-507-4 | Sequence 4, Appli |
| 13 | 41 | 77.4 | 252 | 4 | US-09-198-452A-694 | Sequence 694, App |
| 14 | 37 | 69.8 | 1323 | 1 | US-08-026-138E-4 | Sequence 4, Appli |
| 15 | 37 | 69.8 | 1336 | 2 | US-08-231-193A-58 | Sequence 58, Appl |
| 16 | 37 | 69.8 | 1336 | 2 | US-08-486-273A-58 | Sequence 58, Appl |
| 17 | 37 | 69.8 | 1336 | 3 | US-08-940-086A-58 | Sequence 58, Appl |
| 18 | 37 | 69.8 | 1336 | 3 | US-08-940-035A-58 | Sequence 58, Appl |
| 19 | 37 | 69.8 | 1336 | 3 | US-08-935-105A-58 | Sequence 58, Appl |
| 20 | 37 | 69.8 | 1336 | 4 | US-09-648-797-58 | Sequence 58, Appl |
| 21 | 37 | 69.8 | 1336 | 4 | US-09-386-123-58 | Sequence 58, Appl |
| 22 | 36 | 67.9 | 123 | 4 | US-09-328-352-5925 | Sequence 5925, Ap |
| 23 | 36 | 67.9 | 730 | 4 | US-09-248-796A-15712 | Sequence 15712, A |
| 24 | 35 | 66.0 | 358 | 3 | US-08-858-207A-398 | Sequence 398, App |
| 25 | 35 | 66.0 | 449 | 4 | US-09-583-110-4686 | Sequence 4686, Ap |
| 26 | 34 | 64.2 | 134 | 4 | US-09-489-039A-11592 | Sequence 11592, A |
| 27 | 34 | 64.2 | 409 | 4 | US-09-540-236-2952 | Sequence 2952, Ap |
| 28 | 34 | 64.2 | 1065 | 3 | US-09-412-545-2 | Sequence 2, Appli |
| 29 | 33 | 62.3 | 86 | 4 | US-09-270-767-34956 | Sequence 34956, A |
| 30 | 33 | 62.3 | 86 | 4 | US-09-270-767-50173 | Sequence 50173, A |
| 31 | 33 | 62.3 | 88 | 4 | US-09-328-352-7192 | Sequence 7192, Ap |
| 32 | 33 | 62.3 | 101 | 4 | US-09-248-796A-27320 | Sequence 27320, A |
| 33 | 33 | 62.3 | 176 | 4 | US-09-107-532A-6622 | Sequence 6622, Ap |
| 34 | 33 | 62.3 | 313 | 4 | US-09-551-826D-14 | Sequence 14, Appl |
| 35 | 33 | 62.3 | 340 | 4 | US-09-248-796A-14931 | Sequence 14931, A |
| 36 | 33 | 62.3 | 400 | 4 | US-09-543-681A-4587 | Sequence 4587, Ap |
| 37 | 33 | 62.3 | 452 | 4 | US-09-198-452A-853 | Sequence 853, App |
| 38 | 33 | 62.3 | 556 | 4 | US-09-248-796A-20229 | Sequence 20229, A |
| 39 | 33 | 62.3 | 744 | 4 | US-09-248-796A-17602 | Sequence 17602, A |
| 40 | 33 | 62.3 | 883 | 4 | US-09-489-039A-11249 | Sequence 11249, A |
| 41 | 32 | 60.4 | 68 | 4 | US-09-248-796A-21149 | Sequence 21149, A |
| 42 | 32 | 60.4 | 68 | 4 | US-09-248-796A-22753 | Sequence 22753, A |
| 43 | 32 | 60.4 | 169 | 2 | US-08-895-939-4 | Sequence 4, Appli |
| 44 | 32 | 60.4 | 169 | 3 | US-09-188-820-4 | Sequence 4, Appli |
| 45 | 32 | 60.4 | 169 | 4 | US-09-617-805-7 | Sequence 7, Appli |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 1.57979 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-13
Perfect score: 53
Sequence: 1 FLINPELIVSR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 53 | 100.0 | 11 | 9 | US-09-973-451-13 | Sequence 13, Appl |
| 2 | 53 | 100.0 | 968 | 9 | US-09-973-451-6 | Sequence 6, Appli |
| 3 | 53 | 100.0 | 977 | 9 | US-09-973-451-2 | Sequence 2, Appli |
| 4 | 52 | 98.1 | 976 | 9 | US-09-973-451-4 | Sequence 4, Appli |
| 5 | 42 | 79.2 | 119 | 15 | US-10-424-599-168770 | Sequence 168770, |
| 6 | 42 | 79.2 | 509 | 16 | US-10-437-963-202306 | Sequence 202306, |
| 7 | 42 | 79.2 | 518 | 17 | US-10-425-115-239190 | Sequence 239190, |
| 8 | 42 | 79.2 | 546 | 15 | US-10-425-114-60000 | Sequence 60000, A |
| 9 | 41 | 77.4 | 249 | 15 | US-10-282-122A-54709 | Sequence 54709, A |
| 10 | 41 | 77.4 | 252 | 15 | US-10-289-762-694 | Sequence 694, App |
| 11 | 38 | 71.7 | 59 | 15 | US-10-424-599-215648 | Sequence 215648, |
| 12 | 37 | 69.8 | 1336 | 9 | US-09-945-901-58 | Sequence 58, Appl |
| 13 | 37 | 69.8 | 1336 | 13 | US-10-007-747-58 | Sequence 58, Appl |
| 14 | 37 | 69.8 | 1336 | 14 | US-10-038-937-58 | Sequence 58, Appl |
| 15 | 36 | 67.9 | 107 | 15 | US-10-424-599-183741 | Sequence 183741, |
| 16 | 36 | 67.9 | 473 | 16 | US-10-437-963-124186 | Sequence 124186, |
| 17 | 36 | 67.9 | 519 | 16 | US-10-437-963-124353 | Sequence 124353, |
| 18 | 35 | 66.0 | 449 | 15 | US-10-282-122A-73824 | Sequence 73824, A |
| 19 | 35 | 66.0 | 527 | 14 | US-10-369-493-1735 | Sequence 1735, Ap |
| 20 | 35 | 66.0 | 621 | 14 | US-10-156-761-10025 | Sequence 10025, A |
| 21 | 35 | 66.0 | 820 | 14 | US-10-174-677-30 | Sequence 30, Appl |
| 22 | 35 | 66.0 | 828 | 14 | US-10-174-677-90 | Sequence 90, Appl |
| 23 | 35 | 66.0 | 932 | 14 | US-10-174-677-89 | Sequence 89, Appl |
| 24 | 35 | 66.0 | 932 | 14 | US-10-174-677-91 | Sequence 91, Appl |
| 25 | 34 | 64.2 | 21 | 15 | US-10-663-896-17 | Sequence 17, Appl |
| 26 | 34 | 64.2 | 39 | 15 | US-10-424-599-231144 | Sequence 231144, |
| 27 | 34 | 64.2 | 72 | 15 | US-10-424-599-176489 | Sequence 176489, |
| 28 | 34 | 64.2 | 86 | 15 | US-10-424-599-183835 | Sequence 183835, |
| 29 | 34 | 64.2 | 98 | 15 | US-10-424-599-183834 | Sequence 183834, |
| 30 | 34 | 64.2 | 100 | 15 | US-10-424-599-162739 | Sequence 162739, |
| 31 | 34 | 64.2 | 138 | 10 | US-09-896-580A-8 | Sequence 8, Appli |
| 32 | 34 | 64.2 | 138 | 17 | US-10-340-367-8 | Sequence 8, Appli |
| 33 | 34 | 64.2 | 169 | 10 | US-09-896-580A-3 | Sequence 3, Appli |
| 34 | 34 | 64.2 | 169 | 17 | US-10-340-367-3 | Sequence 3, Appli |
| 35 | 34 | 64.2 | 211 | 15 | US-10-282-122A-47127 | Sequence 47127, A |
| 36 | 34 | 64.2 | 275 | 15 | US-10-424-599-169986 | Sequence 169986, |
| 37 | 34 | 64.2 | 293 | 17 | US-10-425-115-200086 | Sequence 200086, |
| 38 | 34 | 64.2 | 296 | 16 | US-10-474-776-324 | Sequence 324, App |
| 39 | 34 | 64.2 | 307 | 15 | US-10-425-114-58003 | Sequence 58003, A |
| 40 | 34 | 64.2 | 307 | 17 | US-10-425-115-200087 | Sequence 200087, |
| 41 | 34 | 64.2 | 407 | 15 | US-10-282-122A-63173 | Sequence 63173, A |
| 42 | 34 | 64.2 | 408 | 14 | US-10-369-493-3561 | Sequence 3561, Ap |
| 43 | 34 | 64.2 | 449 | 14 | US-10-369-493-20063 | Sequence 20063, A |
| 44 | 34 | 64.2 | 451 | 15 | US-10-282-122A-72152 | Sequence 72152, A |
| 45 | 34 | 64.2 | 523 | 17 | US-10-739-930-8452 | Sequence 8452, Ap |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 0.68617 Seconds
(without alignments)
1546.392 Million cell updates/sec

Title: US-09-973-451-14
Perfect score: 71
Sequence: 1 IALXLPNIXTQPIPLL 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % | | DB | ID | Description |
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| 1 | 67 | 94.4 | 16 | 3 | US-09-302-812-14 | Sequence 14, Appl |
| 2 | 67 | 94.4 | 16 | 3 | US-09-511-477-14 | Sequence 14, Appl |
| 3 | 67 | 94.4 | 16 | 3 | US-09-511-507-14 | Sequence 14, Appl |
| 4 | 65 | 91.5 | 968 | 3 | US-09-302-812-6 | Sequence 6, Appli |
| 5 | 65 | 91.5 | 968 | 3 | US-09-511-477-6 | Sequence 6, Appli |
| 6 | 65 | 91.5 | 968 | 3 | US-09-511-507-6 | Sequence 6, Appli |
| 7 | 65 | 91.5 | 976 | 3 | US-09-302-812-4 | Sequence 4, Appli |
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| 9 | 65 | 91.5 | 976 | 3 | US-09-511-507-4 | Sequence 4, Appli |
| 10 | 65 | 91.5 | 977 | 3 | US-09-302-812-2 | Sequence 2, Appli |
| 11 | 65 | 91.5 | 977 | 3 | US-09-511-477-2 | Sequence 2, Appli |

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|----|------|------|-----|---|----------------------|-------------------|
| 12 | 65 | 91.5 | 977 | 3 | US-09-511-507-2 | Sequence 2, Appli |
| 13 | 46 | 64.8 | 768 | 3 | US-09-302-812-8 | Sequence 8, Appli |
| 14 | 46 | 64.8 | 768 | 3 | US-09-511-477-8 | Sequence 8, Appli |
| 15 | 46 | 64.8 | 768 | 3 | US-09-511-507-8 | Sequence 8, Appli |
| 16 | 41 | 57.7 | 77 | 4 | US-09-248-796A-24036 | Sequence 24036, A |
| 17 | 40 | 56.3 | 160 | 4 | US-09-489-039A-11236 | Sequence 11236, A |
| 18 | 40 | 56.3 | 373 | 3 | US-09-254-077A-12 | Sequence 12, Appl |
| 19 | 38 | 53.5 | 305 | 4 | US-09-270-767-36889 | Sequence 36889, A |
| 20 | 38 | 53.5 | 305 | 4 | US-09-270-767-52106 | Sequence 52106, A |
| 21 | 38 | 53.5 | 342 | 4 | US-09-543-681A-5179 | Sequence 5179, Ap |
| 22 | 38 | 53.5 | 453 | 1 | US-08-439-131A-5 | Sequence 5, Appli |
| 23 | 38 | 53.5 | 453 | 1 | US-08-440-674-4 | Sequence 4, Appli |
| 24 | 38 | 53.5 | 453 | 4 | US-08-879-337-6 | Sequence 6, Appli |
| 25 | 38 | 53.5 | 582 | 4 | US-09-543-681A-4556 | Sequence 4556, Ap |
| 26 | 37 | 52.1 | 143 | 4 | US-09-270-767-37600 | Sequence 37600, A |
| 27 | 37 | 52.1 | 143 | 4 | US-09-270-767-52817 | Sequence 52817, A |
| 28 | 37 | 52.1 | 181 | 4 | US-09-540-236-3607 | Sequence 3607, Ap |
| 29 | 37 | 52.1 | 341 | 4 | US-09-489-039A-8294 | Sequence 8294, Ap |
| 30 | 37 | 52.1 | 366 | 4 | US-09-540-236-3007 | Sequence 3007, Ap |
| 31 | 37 | 52.1 | 415 | 4 | US-09-543-681A-6746 | Sequence 6746, Ap |
| 32 | 37 | 52.1 | 437 | 4 | US-09-489-039A-12063 | Sequence 12063, A |
| 33 | 37 | 52.1 | 542 | 4 | US-09-614-891-10 | Sequence 10, Appl |
| 34 | 37 | 52.1 | 584 | 4 | US-09-489-039A-14137 | Sequence 14137, A |
| 35 | 37 | 52.1 | 597 | 1 | US-08-399-696-102 | Sequence 102, App |
| 36 | 36 | 50.7 | 233 | 4 | US-09-489-039A-12718 | Sequence 12718, A |
| 37 | 36 | 50.7 | 258 | 4 | US-09-248-796A-25815 | Sequence 25815, A |
| 38 | 36 | 50.7 | 331 | 4 | US-09-454-279-12 | Sequence 12, Appl |
| 39 | 36 | 50.7 | 341 | 4 | US-09-543-681A-4713 | Sequence 4713, Ap |
| 40 | 36 | 50.7 | 445 | 4 | US-09-252-991A-22769 | Sequence 22769, A |
| 41 | 36 | 50.7 | 566 | 4 | US-09-252-991A-17972 | Sequence 17972, A |
| 42 | 35.5 | 50.0 | 597 | 4 | US-09-248-796A-14379 | Sequence 14379, A |
| 43 | 35 | 49.3 | 101 | 4 | US-09-345-236B-111 | Sequence 111, App |
| 44 | 35 | 49.3 | 172 | 4 | US-09-270-767-32284 | Sequence 32284, A |
| 45 | 35 | 49.3 | 172 | 4 | US-09-270-767-47501 | Sequence 47501, A |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 2.29787 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-14
Perfect score: 71
Sequence: 1 IALXLPNIXTQPIPLL 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| Result No. | Score | Query Match Length | DB | ID | Description | |
|------------|-------|--------------------|------|----|----------------------|-------------------|
| 1 | 67 | 94.4 | 16 | 9 | US-09-973-451-14 | Sequence 14, Appl |
| 2 | 65 | 91.5 | 968 | 9 | US-09-973-451-6 | Sequence 6, Appli |
| 3 | 65 | 91.5 | 976 | 9 | US-09-973-451-4 | Sequence 4, Appli |
| 4 | 65 | 91.5 | 977 | 9 | US-09-973-451-2 | Sequence 2, Appli |
| 5 | 46 | 64.8 | 768 | 9 | US-09-973-451-8 | Sequence 8, Appli |
| 6 | 43 | 60.6 | 521 | 14 | US-10-278-173-36 | Sequence 36, Appl |
| 7 | 43 | 60.6 | 521 | 14 | US-10-278-536-34 | Sequence 34, Appl |
| 8 | 43 | 60.6 | 521 | 14 | US-10-225-066A-922 | Sequence 922, App |
| 9 | 43 | 60.6 | 521 | 15 | US-10-374-780A-2244 | Sequence 2244, Ap |
| 10 | 43 | 60.6 | 521 | 15 | US-10-412-699B-82 | Sequence 82, Appl |
| 11 | 41 | 57.7 | 79 | 15 | US-10-424-599-182136 | Sequence 182136, |
| 12 | 41 | 57.7 | 96 | 17 | US-10-425-115-302276 | Sequence 302276, |
| 13 | 41 | 57.7 | 499 | 14 | US-10-156-761-9332 | Sequence 9332, Ap |
| 14 | 41 | 57.7 | 1089 | 14 | US-10-369-493-2154 | Sequence 2154, Ap |
| 15 | 41 | 57.7 | 1579 | 9 | US-09-801-368-368 | Sequence 368, App |
| 16 | 41 | 57.7 | 1579 | 14 | US-10-369-493-2000 | Sequence 2000, Ap |
| 17 | 40 | 56.3 | 373 | 9 | US-09-254-077A-12 | Sequence 12, Appl |
| 18 | 40 | 56.3 | 381 | 16 | US-10-437-963-153754 | Sequence 153754, |
| 19 | 40 | 56.3 | 388 | 16 | US-10-437-963-187460 | Sequence 187460, |
| 20 | 40 | 56.3 | 429 | 15 | US-10-282-122A-58079 | Sequence 58079, A |
| 21 | 39 | 54.9 | 134 | 17 | US-10-425-115-275507 | Sequence 275507, |
| 22 | 39 | 54.9 | 228 | 14 | US-10-012-697-1529 | GENERAL INFORMATI |
| 23 | 39 | 54.9 | 1769 | 16 | US-10-437-963-146678 | Sequence 146678, |
| 24 | 38 | 53.5 | 56 | 9 | US-09-796-692-1133 | Sequence 1133, Ap |
| 25 | 38 | 53.5 | 56 | 9 | US-09-796-692-1583 | Sequence 1583, Ap |
| 26 | 38 | 53.5 | 56 | 9 | US-09-796-692-2200 | Sequence 2200, Ap |
| 27 | 38 | 53.5 | 56 | 14 | US-10-040-862-1133 | Sequence 1133, Ap |
| 28 | 38 | 53.5 | 56 | 14 | US-10-040-862-1583 | Sequence 1583, Ap |
| 29 | 38 | 53.5 | 56 | 14 | US-10-040-862-2200 | Sequence 2200, Ap |
| 30 | 38 | 53.5 | 56 | 15 | US-10-057-475B-1133 | Sequence 1133, Ap |
| 31 | 38 | 53.5 | 56 | 15 | US-10-057-475B-1583 | Sequence 1583, Ap |
| 32 | 38 | 53.5 | 56 | 15 | US-10-057-475B-2200 | Sequence 2200, Ap |
| 33 | 38 | 53.5 | 56 | 15 | US-10-154-884B-1133 | Sequence 1133, Ap |
| 34 | 38 | 53.5 | 56 | 15 | US-10-154-884B-1583 | Sequence 1583, Ap |
| 35 | 38 | 53.5 | 56 | 15 | US-10-154-884B-2200 | Sequence 2200, Ap |
| 36 | 38 | 53.5 | 56 | 16 | US-10-764-324-1133 | Sequence 1133, Ap |
| 37 | 38 | 53.5 | 56 | 16 | US-10-764-324-1583 | Sequence 1583, Ap |
| 38 | 38 | 53.5 | 56 | 16 | US-10-764-324-2200 | Sequence 2200, Ap |
| 39 | 38 | 53.5 | 91 | 17 | US-10-425-115-199808 | Sequence 199808, |
| 40 | 38 | 53.5 | 91 | 17 | US-10-425-115-295282 | Sequence 295282, |
| 41 | 38 | 53.5 | 329 | 15 | US-10-282-122A-60939 | Sequence 60939, A |
| 42 | 38 | 53.5 | 348 | 9 | US-09-730-617-2 | Sequence 2, Appli |
| 43 | 38 | 53.5 | 362 | 17 | US-10-425-115-196937 | Sequence 196937, |
| 44 | 38 | 53.5 | 426 | 15 | US-10-282-122A-61195 | Sequence 61195, A |
| 45 | 38 | 53.5 | 430 | 15 | US-10-282-122A-55560 | Sequence 55560, A |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 41.8993 Seconds
 (without alignments)
 1546.392 Million cell updates/sec

Title: US-09-973-451-2
 Perfect score: 5184
 Sequence: 1 MSAGPGCEPCTKRPRWDAAA.....YHAVESCTQTTNQPQRTGA 977

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
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 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|--------|---------|--------|----|-----------------|-------------------|
| | | Match | Length | | | |
| 1 | 5184 | 100.0 | 977 | 3 | US-09-302-812-2 | Sequence 2, Appli |
| 2 | 5184 | 100.0 | 977 | 3 | US-09-511-477-2 | Sequence 2, Appli |
| 3 | 5184 | 100.0 | 977 | 3 | US-09-511-507-2 | Sequence 2, Appli |
| 4 | 4635.5 | 89.4 | 976 | 3 | US-09-302-812-4 | Sequence 4, Appli |
| 5 | 4635.5 | 89.4 | 976 | 3 | US-09-511-477-4 | Sequence 4, Appli |
| 6 | 4635.5 | 89.4 | 976 | 3 | US-09-511-507-4 | Sequence 4, Appli |
| 7 | 4332.5 | 83.6 | 968 | 3 | US-09-302-812-6 | Sequence 6, Appli |
| 8 | 4332.5 | 83.6 | 968 | 3 | US-09-511-477-6 | Sequence 6, Appli |
| 9 | 4332.5 | 83.6 | 968 | 3 | US-09-511-507-6 | Sequence 6, Appli |
| 10 | 1063.5 | 20.5 | 768 | 3 | US-09-302-812-8 | Sequence 8, Appli |
| 11 | 1063.5 | 20.5 | 768 | 3 | US-09-511-477-8 | Sequence 8, Appli |

| | | | | | | |
|----|--------|------|------|---|----------------------|-------------------|
| 12 | 1063.5 | 20.5 | 768 | 3 | US-09-511-507-8 | Sequence 8, Appli |
| 13 | 465 | 9.0 | 726 | 3 | US-09-302-812-10 | Sequence 10, Appl |
| 14 | 465 | 9.0 | 726 | 3 | US-09-511-477-10 | Sequence 10, Appl |
| 15 | 465 | 9.0 | 726 | 3 | US-09-511-507-10 | Sequence 10, Appl |
| 16 | 167 | 3.2 | 31 | 3 | US-09-302-812-11 | Sequence 11, Appl |
| 17 | 167 | 3.2 | 31 | 3 | US-09-511-477-11 | Sequence 11, Appl |
| 18 | 167 | 3.2 | 31 | 3 | US-09-511-507-11 | Sequence 11, Appl |
| 19 | 166 | 3.2 | 1462 | 4 | US-09-538-092-1043 | Sequence 1043, Ap |
| 20 | 155.5 | 3.0 | 1804 | 4 | US-09-362-336A-4 | Sequence 4, Appli |
| 21 | 153 | 3.0 | 913 | 3 | US-08-971-089-4 | Sequence 4, Appli |
| 22 | 152 | 2.9 | 914 | 1 | US-08-484-105-2 | Sequence 2, Appli |
| 23 | 152 | 2.9 | 914 | 1 | US-08-484-106-2 | Sequence 2, Appli |
| 24 | 149.5 | 2.9 | 2224 | 4 | US-09-054-272-38 | Sequence 38, Appl |
| 25 | 149 | 2.9 | 29 | 3 | US-09-302-812-12 | Sequence 12, Appl |
| 26 | 149 | 2.9 | 29 | 3 | US-09-511-477-12 | Sequence 12, Appl |
| 27 | 149 | 2.9 | 29 | 3 | US-09-511-507-12 | Sequence 12, Appl |
| 28 | 147 | 2.8 | 26 | 3 | US-09-302-812-19 | Sequence 19, Appl |
| 29 | 147 | 2.8 | 26 | 3 | US-09-511-477-19 | Sequence 19, Appl |
| 30 | 147 | 2.8 | 26 | 3 | US-09-511-507-19 | Sequence 19, Appl |
| 31 | 147 | 2.8 | 2004 | 4 | US-09-538-092-1371 | Sequence 1371, Ap |
| 32 | 146.5 | 2.8 | 1187 | 1 | US-08-320-559-28 | Sequence 28, Appl |
| 33 | 146.5 | 2.8 | 1187 | 3 | US-08-545-860D-28 | Sequence 28, Appl |
| 34 | 146.5 | 2.8 | 1187 | 5 | PCT-US94-04496-28 | Sequence 28, Appl |
| 35 | 146.5 | 2.8 | 1210 | 1 | US-08-320-559-26 | Sequence 26, Appl |
| 36 | 146.5 | 2.8 | 1210 | 3 | US-08-545-860D-26 | Sequence 26, Appl |
| 37 | 146.5 | 2.8 | 1210 | 4 | US-09-538-092-1179 | Sequence 1179, Ap |
| 38 | 146.5 | 2.8 | 1210 | 5 | PCT-US94-04496-26 | Sequence 26, Appl |
| 39 | 146.5 | 2.8 | 1489 | 4 | US-09-538-092-304 | Sequence 304, App |
| 40 | 146 | 2.8 | 1059 | 4 | US-09-270-767-45764 | Sequence 45764, A |
| 41 | 145.5 | 2.8 | 447 | 4 | US-09-794-422-44 | Sequence 44, Appl |
| 42 | 144 | 2.8 | 598 | 4 | US-09-538-092-1083 | Sequence 1083, Ap |
| 43 | 144 | 2.8 | 601 | 4 | US-09-248-796A-24733 | Sequence 24733, A |
| 44 | 143.5 | 2.8 | 717 | 3 | US-08-910-925-1 | Sequence 1, Appli |
| 45 | 143.5 | 2.8 | 1177 | 3 | US-09-134-001C-5106 | Sequence 5106, Ap |

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 140.314 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-2
Perfect score: 5184
Sequence: 1 MSAGPGCEPCTKRPRWDAAA.....YHAVESCTQTTNQPQRTGA 977

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|--------|----------------|--------|----|----------------------|-------------------|
| 1 | 5184 | 100.0 | 977 | 9 | US-09-973-451-2 | Sequence 2, Appli |
| 2 | 4635.5 | 89.4 | 976 | 9 | US-09-973-451-4 | Sequence 4, Appli |
| 3 | 4332.5 | 83.6 | 968 | 9 | US-09-973-451-6 | Sequence 6, Appli |
| 4 | 1063.5 | 20.5 | 768 | 9 | US-09-973-451-8 | Sequence 8, Appli |
| 5 | 618 | 11.9 | 509 | 16 | US-10-437-963-202306 | Sequence 202306, |
| 6 | 594 | 11.5 | 518 | 17 | US-10-425-115-239190 | Sequence 239190, |
| 7 | 594 | 11.5 | 546 | 15 | US-10-425-114-60000 | Sequence 60000, A |
| 8 | 465 | 9.0 | 726 | 9 | US-09-973-451-10 | Sequence 10, Appl |
| 9 | 205.5 | 4.0 | 200 | 15 | US-10-424-599-184988 | Sequence 184988, |
| 10 | 184 | 3.5 | 180 | 15 | US-10-424-599-156445 | Sequence 156445, |
| 11 | 167 | 3.2 | 31 | 9 | US-09-973-451-11 | Sequence 11, Appl |
| 12 | 166 | 3.2 | 1462 | 14 | US-10-287-218-17 | Sequence 17, Appl |
| 13 | 166 | 3.2 | 1462 | 16 | US-10-408-765A-756 | Sequence 756, App |
| 14 | 166 | 3.2 | 1462 | 16 | US-10-474-291-17 | Sequence 17, Appl |
| 15 | 166 | 3.2 | 1462 | 17 | US-10-473-127-1797 | Sequence 1797, Ap |
| 16 | 166 | 3.2 | 1462 | 17 | US-10-473-127-1798 | Sequence 1798, Ap |
| 17 | 166 | 3.2 | 1462 | 17 | US-10-473-127-1801 | Sequence 1801, Ap |
| 18 | 166 | 3.2 | 1462 | 17 | US-10-473-127-1802 | Sequence 1802, Ap |
| 19 | 164.5 | 3.2 | 300 | 15 | US-10-424-599-233915 | Sequence 233915, |
| 20 | 162.5 | 3.1 | 747 | 15 | US-10-425-114-67803 | Sequence 67803, A |
| 21 | 162.5 | 3.1 | 1109 | 15 | US-10-425-114-72939 | Sequence 72939, A |
| 22 | 162 | 3.1 | 748 | 9 | US-09-864-761-43244 | Sequence 43244, A |
| 23 | 162 | 3.1 | 3394 | 16 | US-10-408-765A-529 | Sequence 529, App |
| 24 | 161 | 3.1 | 691 | 15 | US-10-108-260A-4345 | Sequence 4345, Ap |
| 25 | 160 | 3.1 | 1121 | 16 | US-10-437-963-196036 | Sequence 196036, |
| 26 | 159 | 3.1 | 6642 | 14 | US-10-369-493-5013 | Sequence 5013, Ap |
| 27 | 158.5 | 3.1 | 1973 | 15 | US-10-197-824-34 | Sequence 34, Appl |
| 28 | 158.5 | 3.1 | 2047 | 15 | US-10-346-863-2 | Sequence 2, Appli |
| 29 | 158.5 | 3.1 | 3863 | 15 | US-10-197-824-7 | Sequence 7, Appli |
| 30 | 157.5 | 3.0 | 1163 | 14 | US-10-291-172-197 | Sequence 197, App |
| 31 | 157.5 | 3.0 | 1163 | 15 | US-10-221-278-197 | Sequence 197, App |
| 32 | 156 | 3.0 | 1235 | 17 | US-10-416-330-39 | Sequence 39, Appl |
| 33 | 156 | 3.0 | 2665 | 9 | US-09-864-761-34248 | Sequence 34248, A |
| 34 | 156 | 3.0 | 3664 | 14 | US-10-177-293-423 | Sequence 423, App |
| 35 | 156 | 3.0 | 3664 | 15 | US-10-263-929-143 | Sequence 143, App |
| 36 | 156 | 3.0 | 3664 | 16 | US-10-408-765A-2287 | Sequence 2287, Ap |
| 37 | 156 | 3.0 | 3664 | 17 | US-10-684-422-244 | Sequence 244, App |
| 38 | 155.5 | 3.0 | 566 | 15 | US-10-424-599-172054 | Sequence 172054, |
| 39 | 155.5 | 3.0 | 1001 | 16 | US-10-408-765A-1688 | Sequence 1688, Ap |
| 40 | 155.5 | 3.0 | 1501 | 9 | US-09-924-154-17 | Sequence 17, Appl |
| 41 | 155.5 | 3.0 | 1804 | 14 | US-10-275-140-2 | Sequence 2, Appli |
| 42 | 154 | 3.0 | 406 | 16 | US-10-451-467A-262 | Sequence 262, App |
| 43 | 154 | 3.0 | 612 | 17 | US-10-425-115-247745 | Sequence 247745, |
| 44 | 153 | 3.0 | 913 | 13 | US-10-117-604-4 | Sequence 4, Appli |
| 45 | 152.5 | 2.9 | 460 | 16 | US-10-767-701-42484 | Sequence 42484, A |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 41.8564 Seconds
(without alignments)
1546.392 Million cell updates/sec

Title: US-09-973-451-4
Perfect score: 5190
Sequence: 1 MNAGPGCEPCTKATRWGAAT.....YHAVESCAETADHSGQRTGT 976

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|--------|---------|--------|----|-----------------|-------------------|
| | | Match | Length | | | |
| 1 | 5190 | 100.0 | 976 | 3 | US-09-302-812-4 | Sequence 4, Appli |
| 2 | 5190 | 100.0 | 976 | 3 | US-09-511-477-4 | Sequence 4, Appli |
| 3 | 5190 | 100.0 | 976 | 3 | US-09-511-507-4 | Sequence 4, Appli |
| 4 | 4635.5 | 89.3 | 977 | 3 | US-09-302-812-2 | Sequence 2, Appli |
| 5 | 4635.5 | 89.3 | 977 | 3 | US-09-511-477-2 | Sequence 2, Appli |
| 6 | 4635.5 | 89.3 | 977 | 3 | US-09-511-507-2 | Sequence 2, Appli |
| 7 | 4395 | 84.7 | 968 | 3 | US-09-302-812-6 | Sequence 6, Appli |
| 8 | 4395 | 84.7 | 968 | 3 | US-09-511-477-6 | Sequence 6, Appli |
| 9 | 4395 | 84.7 | 968 | 3 | US-09-511-507-6 | Sequence 6, Appli |
| 10 | 1078 | 20.8 | 768 | 3 | US-09-302-812-8 | Sequence 8, Appli |
| 11 | 1078 | 20.8 | 768 | 3 | US-09-511-477-8 | Sequence 8, Appli |

| | | | | | | |
|----|-------|------|------|---|----------------------|-------------------|
| 12 | 1078 | 20.8 | 768 | 3 | US-09-511-507-8 | Sequence 8, Appli |
| 13 | 463 | 8.9 | 726 | 3 | US-09-302-812-10 | Sequence 10, Appl |
| 14 | 463 | 8.9 | 726 | 3 | US-09-511-477-10 | Sequence 10, Appl |
| 15 | 463 | 8.9 | 726 | 3 | US-09-511-507-10 | Sequence 10, Appl |
| 16 | 167 | 3.2 | 31 | 3 | US-09-302-812-11 | Sequence 11, Appl |
| 17 | 167 | 3.2 | 31 | 3 | US-09-511-477-11 | Sequence 11, Appl |
| 18 | 167 | 3.2 | 31 | 3 | US-09-511-507-11 | Sequence 11, Appl |
| 19 | 163.5 | 3.2 | 601 | 4 | US-09-248-796A-24733 | Sequence 24733, A |
| 20 | 161 | 3.1 | 2375 | 4 | US-09-538-092-1131 | Sequence 1131, Ap |
| 21 | 161 | 3.1 | 2476 | 4 | US-09-824-574-7 | Sequence 7, Appli |
| 22 | 159 | 3.1 | 1462 | 4 | US-09-538-092-1043 | Sequence 1043, Ap |
| 23 | 154 | 3.0 | 1972 | 4 | US-08-875-435B-3 | Sequence 3, Appli |
| 24 | 150.5 | 2.9 | 1177 | 3 | US-09-134-001C-5106 | Sequence 5106, Ap |
| 25 | 150.5 | 2.9 | 1972 | 4 | US-08-875-435B-4 | Sequence 4, Appli |
| 26 | 150 | 2.9 | 3969 | 3 | US-08-061-376-5 | Sequence 5, Appli |
| 27 | 150 | 2.9 | 3969 | 4 | US-09-538-092-1262 | Sequence 1262, Ap |
| 28 | 149.5 | 2.9 | 1187 | 1 | US-08-320-559-28 | Sequence 28, Appl |
| 29 | 149.5 | 2.9 | 1187 | 3 | US-08-545-860D-28 | Sequence 28, Appl |
| 30 | 149.5 | 2.9 | 1187 | 5 | PCT-US94-04496-28 | Sequence 28, Appl |
| 31 | 149.5 | 2.9 | 1210 | 1 | US-08-320-559-26 | Sequence 26, Appl |
| 32 | 149.5 | 2.9 | 1210 | 3 | US-08-545-860D-26 | Sequence 26, Appl |
| 33 | 149.5 | 2.9 | 1210 | 4 | US-09-538-092-1179 | Sequence 1179, Ap |
| 34 | 149.5 | 2.9 | 1210 | 5 | PCT-US94-04496-26 | Sequence 26, Appl |
| 35 | 149 | 2.9 | 26 | 3 | US-09-302-812-20 | Sequence 20, Appl |
| 36 | 149 | 2.9 | 26 | 3 | US-09-511-477-20 | Sequence 20, Appl |
| 37 | 149 | 2.9 | 26 | 3 | US-09-511-507-20 | Sequence 20, Appl |
| 38 | 149 | 2.9 | 29 | 3 | US-09-302-812-12 | Sequence 12, Appl |
| 39 | 149 | 2.9 | 29 | 3 | US-09-511-477-12 | Sequence 12, Appl |
| 40 | 149 | 2.9 | 29 | 3 | US-09-511-507-12 | Sequence 12, Appl |
| 41 | 149 | 2.9 | 427 | 3 | US-09-134-001C-5143 | Sequence 5143, Ap |
| 42 | 147 | 2.8 | 754 | 4 | US-09-976-594-375 | Sequence 375, App |
| 43 | 146.5 | 2.8 | 2125 | 4 | US-09-919-172-29 | Sequence 29, Appl |
| 44 | 146.5 | 2.8 | 2704 | 4 | US-09-538-092-1260 | Sequence 1260, Ap |
| 45 | 144 | 2.8 | 1596 | 4 | US-08-978-277A-4 | Sequence 4, Appli |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 140.17 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-4
Perfect score: 5190
Sequence: 1 MNAGPGCEPCTKATRWGAAT.....YHAVESCAETADHSGQRTGT 976

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 5190 | 100.0 | 976 | 9 | US-09-973-451-4 | Sequence 4, Appli |
| 2 | 4635.5 | 89.3 | 977 | 9 | US-09-973-451-2 | Sequence 2, Appli |
| 3 | 4395 | 84.7 | 968 | 9 | US-09-973-451-6 | Sequence 6, Appli |
| 4 | 1078 | 20.8 | 768 | 9 | US-09-973-451-8 | Sequence 8, Appli |
| 5 | 626 | 12.1 | 509 | 16 | US-10-437-963-202306 | Sequence 202306, |
| 6 | 595 | 11.5 | 518 | 17 | US-10-425-115-239190 | Sequence 239190, |
| 7 | 595 | 11.5 | 546 | 15 | US-10-425-114-60000 | Sequence 60000, A |
| 8 | 463 | 8.9 | 726 | 9 | US-09-973-451-10 | Sequence 10, Appl |
| 9 | 217.5 | 4.2 | 200 | 15 | US-10-424-599-184988 | Sequence 184988, |
| 10 | 188 | 3.6 | 180 | 15 | US-10-424-599-156445 | Sequence 156445, |
| 11 | 179.5 | 3.5 | 300 | 15 | US-10-424-599-233915 | Sequence 233915, |
| 12 | 174 | 3.4 | 3394 | 16 | US-10-408-765A-529 | Sequence 529, App |
| 13 | 173.5 | 3.3 | 748 | 9 | US-09-864-761-43244 | Sequence 43244, A |
| 14 | 167 | 3.2 | 31 | 9 | US-09-973-451-11 | Sequence 11, Appl |
| 15 | 166.5 | 3.2 | 1163 | 14 | US-10-291-172-197 | Sequence 197, App |
| 16 | 166.5 | 3.2 | 1163 | 15 | US-10-221-278-197 | Sequence 197, App |
| 17 | 166.5 | 3.2 | 1641 | 16 | US-10-408-765A-814 | Sequence 814, App |
| 18 | 166.5 | 3.2 | 1641 | 16 | US-10-408-765A-815 | Sequence 815, App |
| 19 | 165.5 | 3.2 | 1274 | 15 | US-10-282-122A-43837 | Sequence 43837, A |
| 20 | 164.5 | 3.2 | 1111 | 9 | US-09-815-242-12955 | Sequence 12955, A |
| 21 | 161 | 3.1 | 2375 | 16 | US-10-408-765A-277 | Sequence 277, App |
| 22 | 161 | 3.1 | 2476 | 10 | US-09-824-574-7 | Sequence 7, Appli |
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| 24 | 159 | 3.1 | 406 | 16 | US-10-451-467A-262 | Sequence 262, App |
| 25 | 159 | 3.1 | 1462 | 14 | US-10-287-218-17 | Sequence 17, Appl |
| 26 | 159 | 3.1 | 1462 | 16 | US-10-408-765A-756 | Sequence 756, App |
| 27 | 159 | 3.1 | 1462 | 16 | US-10-474-291-17 | Sequence 17, Appl |
| 28 | 159 | 3.1 | 1462 | 17 | US-10-473-127-1797 | Sequence 1797, Ap |
| 29 | 159 | 3.1 | 1462 | 17 | US-10-473-127-1798 | Sequence 1798, Ap |
| 30 | 159 | 3.1 | 1462 | 17 | US-10-473-127-1801 | Sequence 1801, Ap |
| 31 | 159 | 3.1 | 1462 | 17 | US-10-473-127-1802 | Sequence 1802, Ap |
| 32 | 159 | 3.1 | 2419 | 16 | US-10-408-765A-2722 | Sequence 2722, Ap |
| 33 | 158.5 | 3.1 | 1948 | 14 | US-10-032-585-7611 | Sequence 7611, Ap |
| 34 | 156.5 | 3.0 | 1297 | 15 | US-10-282-122A-71692 | Sequence 71692, A |
| 35 | 155.5 | 3.0 | 1163 | 10 | US-09-932-257A-3 | Sequence 3, Appli |
| 36 | 155.5 | 3.0 | 1974 | 14 | US-10-369-493-6395 | Sequence 6395, Ap |
| 37 | 154.5 | 3.0 | 498 | 15 | US-10-424-599-196154 | Sequence 196154, |
| 38 | 154.5 | 3.0 | 3225 | 16 | US-10-408-765A-254 | Sequence 254, App |
| 39 | 153 | 2.9 | 6642 | 14 | US-10-369-493-5013 | Sequence 5013, Ap |
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| 41 | 151 | 2.9 | 803 | 16 | US-10-437-963-131456 | Sequence 131456, |
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| 43 | 150.5 | 2.9 | 408 | 15 | US-10-424-599-224071 | Sequence 224071, |
| 44 | 150.5 | 2.9 | 1169 | 15 | US-10-282-122A-71179 | Sequence 71179, A |
| 45 | 150.5 | 2.9 | 1312 | 14 | US-10-369-493-1950 | Sequence 1950, Ap |

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OM protein - protein search, using sw model

Run on: December 16, 2004, 13:55:33 ; Search time 41.5133 Seconds
(without alignments)
1546.392 Million cell updates/sec

Title: US-09-973-451-6
Perfect score: 5164
Sequence: 1 MSAGPGWEPCTKARWGAAGT.....YHAVESSAETTDMPGQKAGT 968

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 5164 | 100.0 | 968 | 3 | US-09-302-812-6 | Sequence 6, Appli |
| 2 | 5164 | 100.0 | 968 | 3 | US-09-511-477-6 | Sequence 6, Appli |
| 3 | 5164 | 100.0 | 968 | 3 | US-09-511-507-6 | Sequence 6, Appli |
| 4 | 4395 | 85.1 | 976 | 3 | US-09-302-812-4 | Sequence 4, Appli |
| 5 | 4395 | 85.1 | 976 | 3 | US-09-511-477-4 | Sequence 4, Appli |
| 6 | 4395 | 85.1 | 976 | 3 | US-09-511-507-4 | Sequence 4, Appli |
| 7 | 4332.5 | 83.9 | 977 | 3 | US-09-302-812-2 | Sequence 2, Appli |
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| 10 | 1074.5 | 20.8 | 768 | 3 | US-09-302-812-8 | Sequence 8, Appli |
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| 12 | 1074.5 | 20.8 | 768 | 3 | US-09-511-507-8 | Sequence 8, Appli |
| 13 | 443.5 | 8.6 | 726 | 3 | US-09-302-812-10 | Sequence 10, Appl |
| 14 | 443.5 | 8.6 | 726 | 3 | US-09-511-477-10 | Sequence 10, Appl |
| 15 | 443.5 | 8.6 | 726 | 3 | US-09-511-507-10 | Sequence 10, Appl |
| 16 | 167 | 3.2 | 31 | 3 | US-09-302-812-11 | Sequence 11, Appl |
| 17 | 167 | 3.2 | 31 | 3 | US-09-511-477-11 | Sequence 11, Appl |
| 18 | 167 | 3.2 | 31 | 3 | US-09-511-507-11 | Sequence 11, Appl |
| 19 | 167 | 3.2 | 1177 | 3 | US-09-134-001C-5106 | Sequence 5106, Ap |
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| 21 | 163.5 | 3.2 | 1187 | 3 | US-08-545-860D-28 | Sequence 28, Appl |
| 22 | 163.5 | 3.2 | 1187 | 5 | PCT-US94-04496-28 | Sequence 28, Appl |
| 23 | 163.5 | 3.2 | 1210 | 1 | US-08-320-559-26 | Sequence 26, Appl |
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| 33 | 150 | 2.9 | 1115 | 3 | US-09-210-288-2 | Sequence 2, Appli |
| 34 | 150 | 2.9 | 1115 | 6 | 5198347-6 | Patent No. 5198347 |
| 35 | 146 | 2.8 | 3924 | 4 | US-09-538-092-1246 | Sequence 1246, Ap |
| 36 | 145.5 | 2.8 | 559 | 1 | US-08-320-559-31 | Sequence 31, Appl |
| 37 | 145.5 | 2.8 | 559 | 3 | US-08-545-860D-31 | Sequence 31, Appl |
| 38 | 145.5 | 2.8 | 559 | 4 | US-09-538-092-1261 | Sequence 1261, Ap |
| 39 | 145.5 | 2.8 | 559 | 5 | PCT-US94-04496-31 | Sequence 31, Appl |
| 40 | 144 | 2.8 | 26 | 3 | US-09-302-812-21 | Sequence 21, Appl |
| 41 | 144 | 2.8 | 26 | 3 | US-09-511-477-21 | Sequence 21, Appl |
| 42 | 144 | 2.8 | 26 | 3 | US-09-511-507-21 | Sequence 21, Appl |
| 43 | 144 | 2.8 | 29 | 3 | US-09-302-812-12 | Sequence 12, Appl |
| 44 | 144 | 2.8 | 29 | 3 | US-09-511-477-12 | Sequence 12, Appl |
| 45 | 144 | 2.8 | 29 | 3 | US-09-511-507-12 | Sequence 12, Appl |

OM protein - protein search, using sw model

Run on: December 16, 2004, 14:04:49 ; Search time 139.021 Seconds
(without alignments)
2491.591 Million cell updates/sec

Title: US-09-973-451-6
Perfect score: 5164
Sequence: 1 MSAGPGWEPCTKARWGAAGT.....YHAVESSAETTDMPGQKAGT 968

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|--------|----------------|--------|----|----------------------|-------------------|
| 1 | 5164 | 100.0 | 968 | 9 | US-09-973-451-6 | Sequence 6, Appli |
| 2 | 4395 | 85.1 | 976 | 9 | US-09-973-451-4 | Sequence 4, Appli |
| 3 | 4332.5 | 83.9 | 977 | 9 | US-09-973-451-2 | Sequence 2, Appli |
| 4 | 1074.5 | 20.8 | 768 | 9 | US-09-973-451-8 | Sequence 8, Appli |
| 5 | 609 | 11.8 | 509 | 16 | US-10-437-963-202306 | Sequence 202306, |
| 6 | 579 | 11.2 | 518 | 17 | US-10-425-115-239190 | Sequence 239190, |
| 7 | 579 | 11.2 | 546 | 15 | US-10-425-114-60000 | Sequence 60000, A |
| 8 | 443.5 | 8.6 | 726 | 9 | US-09-973-451-10 | Sequence 10, Appl |
| 9 | 220.5 | 4.3 | 200 | 15 | US-10-424-599-184988 | Sequence 184988, |
| 10 | 176 | 3.4 | 6642 | 14 | US-10-369-493-5013 | Sequence 5013, Ap |
| 11 | 175 | 3.4 | 180 | 15 | US-10-424-599-156445 | Sequence 156445, |
| 12 | 172.5 | 3.3 | 300 | 15 | US-10-424-599-233915 | Sequence 233915, |
| 13 | 172 | 3.3 | 1489 | 14 | US-10-115-482-18 | Sequence 18, Appl |
| 14 | 169.5 | 3.3 | 1297 | 15 | US-10-282-122A-71692 | Sequence 71692, A |
| 15 | 167 | 3.2 | 31 | 9 | US-09-973-451-11 | Sequence 11, Appl |
| 16 | 167 | 3.2 | 1169 | 15 | US-10-282-122A-71179 | Sequence 71179, A |
| 17 | 165.5 | 3.2 | 787 | 16 | US-10-473-576-23 | Sequence 23, Appl |
| 18 | 164.5 | 3.2 | 805 | 16 | US-10-473-576-13 | Sequence 13, Appl |
| 19 | 163.5 | 3.2 | 1210 | 14 | US-10-205-823-264 | Sequence 264, App |
| 20 | 161 | 3.1 | 748 | 9 | US-09-864-761-43244 | Sequence 43244, A |
| 21 | 161 | 3.1 | 3394 | 16 | US-10-408-765A-529 | Sequence 529, App |
| 22 | 159.5 | 3.1 | 1501 | 9 | US-09-924-154-17 | Sequence 17, Appl |
| 23 | 159 | 3.1 | 1462 | 14 | US-10-287-218-17 | Sequence 17, Appl |
| 24 | 159 | 3.1 | 1462 | 16 | US-10-408-765A-756 | Sequence 756, App |
| 25 | 159 | 3.1 | 1462 | 16 | US-10-474-291-17 | Sequence 17, Appl |
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| 27 | 159 | 3.1 | 1462 | 17 | US-10-473-127-1798 | Sequence 1798, Ap |
| 28 | 159 | 3.1 | 1462 | 17 | US-10-473-127-1801 | Sequence 1801, Ap |
| 29 | 159 | 3.1 | 1462 | 17 | US-10-473-127-1802 | Sequence 1802, Ap |
| 30 | 159 | 3.1 | 2677 | 14 | US-10-144-194A-22 | Sequence 22, Appl |
| 31 | 159 | 3.1 | 2677 | 17 | US-10-491-566-22 | Sequence 22, Appl |
| 32 | 159 | 3.1 | 2697 | 14 | US-10-144-198-12 | Sequence 12, Appl |
| 33 | 158.5 | 3.1 | 4723 | 14 | US-10-359-012-8 | Sequence 8, Appli |
| 34 | 156 | 3.0 | 691 | 15 | US-10-108-260A-4345 | Sequence 4345, Ap |
| 35 | 152.5 | 3.0 | 406 | 16 | US-10-451-467A-262 | Sequence 262, App |
| 36 | 152 | 2.9 | 1413 | 16 | US-10-437-963-138262 | Sequence 138262, |
| 37 | 151.5 | 2.9 | 1027 | 16 | US-10-437-963-161202 | Sequence 161202, |
| 38 | 150 | 2.9 | 447 | 10 | US-09-794-422-44 | Sequence 44, Appl |
| 39 | 150 | 2.9 | 1115 | 13 | US-10-153-273-2 | Sequence 2, Appli |
| 40 | 149.5 | 2.9 | 894 | 17 | US-10-483-512-33 | Sequence 33, Appl |
| 41 | 148 | 2.9 | 1030 | 16 | US-10-741-601-487 | Sequence 487, App |
| 42 | 148 | 2.9 | 1389 | 15 | US-10-282-122A-70151 | Sequence 70151, A |
| 43 | 147.5 | 2.9 | 1358 | 14 | US-10-369-493-1658 | Sequence 1658, Ap |
| 44 | 147.5 | 2.9 | 1973 | 15 | US-10-197-824-34 | Sequence 34, Appl |
| 45 | 147.5 | 2.9 | 2047 | 15 | US-10-346-863-2 | Sequence 2, Appli |